

PCT

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/743,492

DATE: 03/07/2001
 TIME: 11:36:19

Input Set : A:\37023.txt
 Output Set: N:\CRF3\03072001\I743492.raw

P.S

3 <110> APPLICANT: YAMAMOTO, Hiroshi
 4 TSUJIKAWA, Kazutake
 5 UCHINO, Yukiko
 7 <120> TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR INTRACELLULAR DOMAIN OF PROTEIN
 8 TYROSINE PHOSPHATASE
 10 <130> FILE REFERENCE: 19036/37023
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/743,492
 C--> 13 <141> CURRENT FILING DATE: 2001-01-10
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP98/03120
 16 <151> PRIOR FILING DATE: 1998-07-10
 18 <160> NUMBER OF SEQ ID NOS: 8
 20 <170> SOFTWARE: PatentIn Ver. 2.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 3467
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (6)..(1826)
 31 <220> FEATURE:
 32 <221> NAME/KEY: misc_feature
 33 <222> LOCATION: (213)..(953)
 34 <223> OTHER INFORMATION: Tyrosine Phosphatase Domain 1
 36 <220> FEATURE:
 37 <221> NAME/KEY: misc_feature
 38 <222> LOCATION: (1080)..(1826)
 39 <223> OTHER INFORMATION: Tyrosine Phosphatase Domain 2
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Unknown Organism: Signature Motif
 43 Conserved in Phosphatase Domain of Known PTPs.
 45 <300> PUBLICATION INFORMATION:
 46 <308> DATABASE ACCESSION NO: DDBJ/EMBL/GenBank Accession No. Y00815
 47 <309> DATABASE ENTRY DATE: 1995-09-19
 51 <400> SEQUENCE: 1
 52 gatcc gga ctg aag gac tcc ttg ctg gcc cac tcc tct gac cct gtg gag 50
 53 Gly Leu Lys Asp Ser Leu Leu Ala His Ser Ser Asp Pro Val Glu
 54 1 5 10 15
 56 atg cgg agg ctc aac tac cag acc cca ggt atg cga gac cac cca ccc 98
 57 Met Arg Arg Leu Asn Tyr Gln Thr Pro Gly Met Arg Asp His Pro Pro
 58 20 25 30
 60 atc ccc atc acc gac ctg gcg gac aac atc gag cgc ctc aaa gcc aac 146
 61 Ile Pro Ile Thr Asp Leu Ala Asp Asn Ile Glu Arg Leu Lys Ala Asn
 62 35 40 45
 64 gat ggc ctc aag ttc tcc cag gag tat gag tcc atc gac cct gga cag 194
 65 Asp Gly Leu Lys Phe Ser Gln Glu Tyr Glu Ser Ile Asp Pro Gly Gln
 66 50 55 60
 68 cag ttc acg tgg gag aat tca aac ctg gag gtg aac aag ccc aag aac 242

ENTERED

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69 Gln Phe Thr Trp Glu Asn Ser Asn Leu Glu Val Asn Lys Pro Lys Asn
70      65      70      75
72 cgc tat gcg aat gtc atc gcc tac gac cac tct cga gtc atc ctt acc 290
73 Arg Tyr Ala Asn Val Ile Ala Tyr Asp His Ser Arg Val Ile Leu Thr
74 80      85      90      95
76 tct atc gat ggc gtc ccc ggg agt gac tac atc aat gcc aac tac atc 338
77 Ser Ile Asp Gly Val Pro Gly Ser Asp Tyr Ile Asn Ala Asn Tyr Ile
78      100      105      110
80 gat ggc tac cgc aag cag aat gcc tac atc gcc acg cag ggc ccc ctg 386
81 Asp Gly Tyr Arg Lys Gln Asn Ala Tyr Ile Ala Thr Gln Gly Pro Leu
82      115      120      125
84 ccc gag acc atg ggc gat ttc tgg aga atg gtg tgg gaa cag cgc acg 434
85 Pro Glu Thr Met Gly Asp Phe Trp Arg Met Val Trp Glu Gln Arg Thr
86      130      135      140
88 gcc act gtg gtc atg atg aca cgg ctg gag gag aag tcc cgg gta aaa 482
89 Ala Thr Val Val Met Met Thr Arg Leu Glu Glu Lys Ser Arg Val Lys
90      145      150      155
92 tgt gat cag tac tgg cca gcc cgt ggc acc gag acc tgt ggc ctt att 530
93 Cys Asp Gln Tyr Trp Pro Ala Arg Gly Thr Glu Thr Cys Gly Leu Ile
94 160      165      170      175
96 cag gtg acc ctg ttg gac aca gtg gag ctg gcc aca tac act gtg cgc 578
97 Gln Val Thr Leu Leu Asp Thr Val Glu Leu Ala Thr Tyr Thr Val Arg
98      180      185      190
100 acc ttc gca ctc cac aag agt ggc tcc agt gag aag cgt gag ctg cgt 626
101 Thr Phe Ala Leu His Lys Ser Gly Ser Ser Glu Lys Arg Glu Leu Arg
102      195      200      205
104 cag ttt cag ttc atg gcc tgg cca gac cat gga gtt cct gag tac cca 674
105 Gln Phe Gln Phe Met Ala Trp Pro Asp His Gly Val Pro Glu Tyr Pro
106      210      215      220
108 act ccc atc ctg gcc ttc cta cga cgg gtc aag gcc tgc aac ccc cta 722
109 Thr Pro Ile Leu Ala Phe Leu Arg Arg Val Lys Ala Cys Asn Pro Leu
110      225      230      235
112 gac gca ggg ccc atg gtg gtg cac tgc agc gcg ggc gtg ggc cgc acc 770
113 Asp Ala Gly Pro Met Val Val His Cys Ser Ala Gly Val Gly Arg Thr
114 240      245      250      255
116 ggc tgc ttc atc gtg att gat gcc atg ttg gag cgg atg aag cac gag 818
117 Gly Cys Phe Ile Val Ile Asp Ala Met Leu Glu Arg Met Lys His Glu
118      260      265      270
120 aag acg gtg gac atc tat ggc cac gtg acc tgc atg cga tca cag agg 866
121 Lys Thr Val Asp Ile Tyr Gly His Val Thr Cys Met Arg Ser Gln Arg
122      275      280      285
124 aac tac atg gtg cag acg gag gac cag tac gtg ttc atc cat gag gcg 914
125 Asn Tyr Met Val Gln Thr Glu Asp Gln Tyr Val Phe Ile His Glu Ala
126      290      295      300
128 ctg ctg gag gct gcc acg tgc ggc cac aca gag gtg cct gcc cgc aac 962
129 Leu Leu Glu Ala Ala Thr Cys Gly His Thr Glu Val Pro Ala Arg Asn
130      305      310      315
132 ctg tat gcc cac atc cag aag ctg ggc caa gtg cct cca ggg gag agt 1010
133 Leu Tyr Ala His Ile Gln Lys Leu Gly Gln Val Pro Pro Gly Glu Ser

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134	320		325		330		335	
136	gtg acc gcc atg gag ctc gag ttc aag ttg ctg gcc agc tcc aag gcc	1058						
137	Val Thr Ala Met Glu Leu Glu Phe Lys Leu Leu Ala Ser Ser Lys Ala							
138			340		345		350	
140	cac acg tcc cgc ttc atc agc gcc aac ctg ccc tgc aac aag ttc aag	1106						
141	His Thr Ser Arg Phe Ile Ser Ala Asn Leu Pro Cys Asn Lys Phe Lys							
142			355		360		365	
144	aac cgg ctg gtg aac atc atg ccc tac gaa ttg acc cgt gtg tgt ctg	1154						
145	Asn Arg Leu Val Asn Ile Met Pro Tyr Glu Leu Thr Arg Val Cys Leu							
146			370		375		380	
148	cag ccc atc cgt ggt gtg gag ggc tct gac tac atc aat gcc agc ttc	1202						
149	Gln Pro Ile Arg Gly Val Glu Gly Ser Asp Tyr Ile Asn Ala Ser Phe							
150			385		390		395	
152	ctg gat ggt tat aga cag cag aag gcc tac ata gct aca cag ggg cct	1250						
153	Leu Asp Gly Tyr Arg Gln Lys Ala Tyr Ile Ala Thr Gln Gly Pro							
154	400		405		410		415	
156	ctg gca gag agc acc gag gac ttc tgg cgc atg cta tgg gag cac aat	1298						
157	Leu Ala Glu Ser Thr Glu Asp Phe Trp Arg Met Leu Trp Glu His Asn							
158			420		425		430	
160	tcc acc atc atc gtc atg ctg acc aag ctt cgg gag atg ggc agg gag	1346						
161	Ser Thr Ile Ile Val Met Leu Thr Lys Leu Arg Glu Met Gly Arg Glu							
162			435		440		445	
164	aaa tgc cac cag tac tgg cca gca gag cgc tct gct cgc tac cag tac	1394						
165	Lys Cys His Gln Tyr Trp Pro Ala Glu Arg Ser Ala Arg Tyr Gln Tyr							
166			450		455		460	
168	ttt gtt gtt gac cgg atg gct gag tac aac atg ccc cag tat atc ctg	1442						
169	Phe Val Val Asp Pro Met Ala Glu Tyr Asn Met Pro Gln Tyr Ile Leu							
170			465		470		475	
172	cgt gag ttc aag gtc acg gat gcc cgg gat ggg cag tca agg aca atc	1490						
173	Arg Glu Phe Lys Val Thr Asp Ala Arg Asp Gly Gln Ser Arg Thr Ile							
174	480		485		490		495	
176	cgg cag ttc cag ttc aca gac tgg cca gag cag ggc gtg ccc aag aca	1538						
177	Arg Gln Phe Gln Phe Thr Asp Trp Pro Glu Gln Gly Val Pro Lys Thr							
178			500		505		510	
180	ggc gag gga ttc att gac ttc atc ggg cag gtg cat aag acc aag gag	1586						
181	Gly Glu Gly Phe Ile Asp Phe Ile Gly Gln Val His Lys Thr Lys Glu							
182			515		520		525	
184	cag ttt gga cag gat ggg cct atc acg gtg cac tgc agt gct ggc gtg	1634						
185	Gln Phe Gly Gln Asp Gly Pro Ile Thr Val His Cys Ser Ala Gly Val							
186			530		535		540	
188	ggc cgc acc ggg gtg ttc atc act ctg agc atc gtc ctg gag cgc atg	1682						
189	Gly Arg Thr Gly Val Phe Ile Thr Leu Ser Ile Val Leu Glu Arg Met							
190			545		550		555	
192	cgc tat gag ggc gtg gtc gac atg ttt cag acc gtg aag acc ctg cgt	1730						
193	Arg Tyr Glu Gly Val Val Asp Met Phe Gln Thr Val Lys Thr Leu Arg							
194	560		565		570		575	
196	aca cag cgt cct gcc atg gtg cag aca gag gac cag tat cag ctg tgc	1778						
197	Thr Gln Arg Pro Ala Met Val Gln Thr Glu Asp Gln Tyr Gln Leu Cys							
198			580		585		590	

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200 tac cgt gcg gcc ctg gag tac ctc ggc agc ttt gac cac tat gca acg 1826
201 Tyr Arg Ala Ala Leu Glu Tyr Leu Gly Ser Phe Asp His Tyr Ala Thr
202          595          600          605
204 taactaccgc tccctctccc tccgccaccc ccgccgtggg gctccggagg ggaccagct 1886
206 cctctgagcc ataccgacca tcgtccagcc ctccctacgca gatgctgtca ctggcagagc 1946
208 acagcccacg gggatcacag cgtttcagga acgttgccac accaatcaga gagcctagaa 2006
210 catccctggg caagtggagt gcccgacagg caggcaactgt ggcccttctg tccaccagac 2066
212 ccacctggag ccgcgttcaa gctctctgtt gcgctccgcg atttctcatg cttcttctca 2126
214 tgggggtggg ttggggcaaa gcctcctttt taatacatta agtggggtag actgagggat 2186
216 tttagcctct tccctctgat ttttctttc gcgaatccgt atctgcagaa tgggccactg 2246
218 taggggttgg ggtttatttt gttttgtttt tttttttttt ttgtatgact tctgtgaag 2306
220 gacagaacat tgccttcctc gtgcagagct ggggctgcca gcctgagcgg aggcctggcc 2366
222 gtgggcccgg aggcagtgtc gatccggctg ctccctccagc ctttcagacg agatcctgtt 2426
224 tcagctaaat gcagggaac tcaatgtttt ttttaagttt gttttccctt taaagccttt 2486
226 ttttaggcca cattgacagt ggtgggcggg gagaagatag ggaacactca tccctggtcg 2546
228 tctatcccag tgtgtgttta acattcacag cccagaacca cagatgtgtc tgggagagcc 2606
230 tggcaaggca ttctcatca ccatcgtgtt tgcaaagggt aaaacaaaaa caaaaaacca 2666
232 caaaaataaa aaacaaaaaa aacaaaaaac caaaaaaaaa aaaaaaaaag agtcagccct 2726
234 tggcttctgc ttcaaaccct caagagggga agcaactccg tgtgcctggg gttcccagg 2786
236 gagctgctgg ctgacctggg cccacagagc ctggctttgg tcccagcat tgcagtatgg 2846
238 tgtggtgttt gtaggctgtg ggtcttggt gtgtggccaa ggtgaatagc acaggttagg 2906
240 gtgtgtgcca caccctatgc acctcagggc caagcggggg cgtggctggc ctttcaggtc 2966
242 caggccagtg ggccgtgtag cacatgtctg tcctcagagc aggggccaga tgattttcct 3026
244 ccttggtttg cagctgtttt caaagcccc gataatcgct cttttccact ccaagatgcc 3086
246 ctcataaacc aatgtggcaa gactactgga cttctatcaa tggtaactta atcagtcctt 3146
248 attatcccag cttgctgagg ggcagggaga gcgcctcttc ctctgggcag cgctatctag 3206
250 ataggtaagt gggggcgggg aagggtgcat agctgtttta gctgagggac gtggtgccga 3266
252 cgtccccaac ctagctagg ctaagtcaag atcaacattc cagggttggg aatgttggat 3326
254 gatgaaacat tcatttttac cttgtggatg ctagtgtgt agagtccact gttgtacaca 3386
256 gtctgttttc tatttggtta gaaaaactac agcatcattg cataattctt gatggtaata 3446
258 aatttgaata atcagatttc t                                     3467
262 <210> SEQ ID NO: 2
263 <211> LENGTH: 11
264 <212> TYPE: PRT
265 <213> ORGANISM: Unknown
267 <220> FEATURE:
268 <223> OTHER INFORMATION: Description of Unknown Organism: Signature Motif
269     Conserved in Phosphatase Domain of Known PTPs.
271 <220> FEATURE:
272 <221> NAME/KEY: SITE
273 <222> LOCATION: (1)
274 <223> OTHER INFORMATION: Xaa = Ile or Val
276 <220> FEATURE:
277 <221> NAME/KEY: SITE
278 <222> LOCATION: (10)
279 <223> OTHER INFORMATION: Xaa= Ser of Thr
281 <220> FEATURE:
282 <221> NAME/KEY: SITE
283 <222> LOCATION: (4)

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284 <223> OTHER INFORMATION: Xaa= Unknown
286 <220> FEATURE:
287 <221> NAME/KEY: SITE
288 <222> LOCATION: (7)..(8)
289 <223> OTHER INFORMATION: Xaa= Unknown
291 <400> SEQUENCE: 2
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293      1          5          10
296 <210> SEQ ID NO: 3
297 <211> LENGTH: 7702
298 <212> TYPE: DNA
299 <213> ORGANISM: Homo sapiens
301 <220> FEATURE:
302 <221> NAME/KEY: CDS
303 <222> LOCATION: (371)..(6061)
305 <220> FEATURE:
306 <221> NAME/KEY: sig_peptide
307 <222> LOCATION: (371)..(418)
309 <220> FEATURE:
310 <221> NAME/KEY: mat_peptide
311 <222> LOCATION: (419)..(6061)
313 <220> FEATURE:
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315 <222> LOCATION: (419)..(4120)
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318 <220> FEATURE:
319 <221> NAME/KEY: misc_feature
320 <222> LOCATION: (4121)..(4192)
321 <223> OTHER INFORMATION: Transmembrane Domain
323 <220> FEATURE:
324 <221> NAME/KEY: misc_feature
325 <222> LOCATION: (4193)..(6061)
326 <223> OTHER INFORMATION: Cytoplasmic Domain
328 <300> PUBLICATION INFORMATION:
329 <308> DATABASE ACCESSION NO: DDBJ/EMBL/GenBank Accession No. Y00815
330 <309> DATABASE ENTRY DATE: 1995-09-19
332 <400> SEQUENCE: 3
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335 gggctcgggc tccggctccg gctccggctc cggctccagc tcgggtggcg gtggcgggag 120
337 cgggaccagg tggaggcggc ggccggcagag gaggggagc agcggcccta gcggcttgcg 180
339 gggggacatg cggaccgacg gccctggat agcgggaagg agtggaggcc ctggtgcccg 240
341 gcccttggtg ctgagtatcc agcaagagtg accggggtga agaagcaaag actcggttga 300
343 ttgtcctggg ctgtggctgg ctgtggagct agagccctgg atggccctg agccagcccc 360
345 agggaggacg atg gtg ccc ctt gtg cct gca ctg gtg atg ctt ggt ttg 409
346      Met Val Pro Leu Val Pro Ala Leu Val Met Leu Gly Leu
347      -15          -10          -5
349 gtg gca ggc gcc cat ggt gac agc aaa cct gtc ttc att aaa gtc cct 457
350 Val Ala Gly Ala His Gly Asp Ser Lys Pro Val Phe Ile Lys Val Pro
351      -1  1          5          10

```

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:916 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:940 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1003 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8